

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/830,844
Source: PCT
Date Processed by STIC: 4-19-05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

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Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER

10/530,844

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics Wrapped Amino The number(s) at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5' amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence(s).

8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown, or is Artificial Sequence.

11 Use of <220>

Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section (See "Federal Register," 00701/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)

12 PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/530,844

DATE: 04/19/2005

TIME: 08:46:17

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

5 <110> APPLICANT: Consortium for elektrochemische Industrie GmbH
 9 <120> TITLE OF INVENTION: Feedback-resistente Homoserin-Transsuccinylasen mit
 11 modifiziertem C-Terminus
 15 <130> FILE REFERENCE: Co10221
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/10/530,844
 C--> 20 <141> CURRENT FILING DATE: 2005-04-08
 24 <160> NUMBER OF SEQ ID NOS: 12
 28 <170> SOFTWARE: PatentIn Ver. 2.0
 32 <210> SEQ ID NO: 1
 34 <211> LENGTH: 930
 36 <212> TYPE: DNA
 38 <213> ORGANISM: Escherichia coli
 42 <220> FEATURE:
 44 <221> NAME/KEY: CDS
 46 <222> LOCATION: (1)..(930)
 50 <300> PUBLICATION INFORMATION:
 52 <301> AUTHORS: Blattner, F. R.
 54 <302> TITLE: The complete genome sequence of Escherichia coli K-12.
 56 <303> JOURNAL: Science
 58 <304> VOLUME: 277
 60 <305> ISSUE: 533
 62 <306> PAGES: 1453-1474
 64 <307> DATE: 1997
 66 <308> DATABASE ACCESSION NO: Blattner, F.R.
 W--> 70 <309> PUBLICATION INFORMATION: 1
 72 atg ccg att cgt gtg ccg gac gag cta ccc gcc gtc aat ttc ttg cgt 48
 74 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
 76 1 5 10 15
 80 gaa gaa aac gtc ttt gtg atg aca act tct cgt gcg tct ggt cag gaa 96
 82 Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
 84 20 25 30
 88 att cgt cca ctt aag gtt ctg atc ctt aac ctg atg ccg aag aag att 144
 90 Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
 92 35 40 45
 96 gaa act gaa aat cag ttt ctg cgc ctg ctt tca aac tca cct ttg cag 192
 98 Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
 100 50 55 60
 104 gtc gat att cag ctg ttg cgc atc gat tcc cgt gaa tcg cgc aac acg 240
 106 Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
 108 65 70 75 80
 112 ccc gca gag cat ctg aac aac ttc tac tgt aac ttt gaa gat att cag 288
 114 Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
 116 85 90 95

pls do not use
 foreign language in
 U.S. Applications.
 Does Not Comply
 Corrected Diskette Needed
 (pg. 1-5)

Mandatory, if <308>
 is shown, then
 <309>
 must be
 inserted.

RAW SEQUENCE LISTING

DATE: 04/19/2005

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TIME: 08:46:17

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

```

120 gat cag aac ttt gac ggt ttg att gta act ggt gcg ccg ctg ggc ctg 336
122 Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
124      100      105      110
128 gtg gag ttt aat gat gtc gct tac tgg ccg cag atc aaa cag gtg ctg 384
130 Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
132      115      120      125
136 gag tgg tcg aaa gat cac gtc acc tcg acg ctg ttt gtc tgc tgg gcg 432
138 Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
140      130      135      140
144 gta cag gcc gcg ctc aat atc ctc tac ggc att cct aag caa act cgc 480
146 Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
148 145      150      155      160
152 acc gaa aaa ctc tct ggc gtt tac gag cat cat att ctc cat cct cat 528
154 Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
156      165      170      175
160 gcg ctt ctg acg cgt ggc ttt gat gat tca ttc ctg gca ccg cat tcg 576
162 Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
164      180      185      190
168 cgc tat gct gac ttt ccg gca gcg ttg att cgt gat tac acc gat ctg 624
170 Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
172      195      200      205
176 gaa att ctg gca gag acg gaa gaa ggg gat gca tat ctg ttt gcc agt 672
178 Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
180      210      215      220
184 aaa gat aag cgc att gcc ttt gtg acg ggc cat ccc gaa tat gat gcg 720
186 Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
188 225      230      235      240
192 caa acg ctg gcg cag gaa ttt ttc cgc gat gtg gaa gcc gga cta gac 768
194 Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
196      245      250      255
200 ccg gat gta ccg tat aac tat ttc ccg cac aat gat ccg caa aat aca 816
202 Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
204      260      265      270
208 ccg cga gcg agc tgg cgt agt cac ggt aat tta ctg ttt acc aac tgg 864
210 Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
212      275      280      285
216 ctc aac tat tac gtc tac cag atc acg cca tac gat cta cgg cac atg 912
218 Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
220      290      295      300
224 aat cca acg ctg gat taa 930
226 Asn Pro Thr Leu Asp
W--> 228 305
234 <210> SEQ ID NO: 2
236 <211> LENGTH: 309
238 <212> TYPE: PRT
240 <213> ORGANISM: Escherichia coli
244 <400> SEQUENCE: 2
246 Met Pro Ile Arg Val Pro Asp Glu Leu Pro Ala Val Asn Phe Leu Arg
248 1 5 10 15

```

310 delete

RAW SEQUENCE LISTING

DATE: 04/19/2005

PATENT APPLICATION: US/10/530,844

TIME: 08:46:17

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

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252 Glu Glu Asn Val Phe Val Met Thr Thr Ser Arg Ala Ser Gly Gln Glu
254           20           25           30
258 Ile Arg Pro Leu Lys Val Leu Ile Leu Asn Leu Met Pro Lys Lys Ile
260           35           40           45
264 Glu Thr Glu Asn Gln Phe Leu Arg Leu Leu Ser Asn Ser Pro Leu Gln
266           50           55           60
270 Val Asp Ile Gln Leu Leu Arg Ile Asp Ser Arg Glu Ser Arg Asn Thr
272           65           70           75           80
276 Pro Ala Glu His Leu Asn Asn Phe Tyr Cys Asn Phe Glu Asp Ile Gln
278           85           90           95
282 Asp Gln Asn Phe Asp Gly Leu Ile Val Thr Gly Ala Pro Leu Gly Leu
284           100          105          110
288 Val Glu Phe Asn Asp Val Ala Tyr Trp Pro Gln Ile Lys Gln Val Leu
290           115          120          125
294 Glu Trp Ser Lys Asp His Val Thr Ser Thr Leu Phe Val Cys Trp Ala
296           130          135          140
300 Val Gln Ala Ala Leu Asn Ile Leu Tyr Gly Ile Pro Lys Gln Thr Arg
302           145          150          155          160
306 Thr Glu Lys Leu Ser Gly Val Tyr Glu His His Ile Leu His Pro His
308           165          170          175
312 Ala Leu Leu Thr Arg Gly Phe Asp Asp Ser Phe Leu Ala Pro His Ser
314           180          185          190
318 Arg Tyr Ala Asp Phe Pro Ala Ala Leu Ile Arg Asp Tyr Thr Asp Leu
320           195          200          205
324 Glu Ile Leu Ala Glu Thr Glu Glu Gly Asp Ala Tyr Leu Phe Ala Ser
326           210          215          220
330 Lys Asp Lys Arg Ile Ala Phe Val Thr Gly His Pro Glu Tyr Asp Ala
332           225          230          235          240
336 Gln Thr Leu Ala Gln Glu Phe Phe Arg Asp Val Glu Ala Gly Leu Asp
338           245          250          255
342 Pro Asp Val Pro Tyr Asn Tyr Phe Pro His Asn Asp Pro Gln Asn Thr
344           260          265          270
348 Pro Arg Ala Ser Trp Arg Ser His Gly Asn Leu Leu Phe Thr Asn Trp
350           275          280          285
354 Leu Asn Tyr Tyr Val Tyr Gln Ile Thr Pro Tyr Asp Leu Arg His Met
356           290          295          300
360 Asn Pro Thr Leu Asp

```

362 305

368 <210> SEQ ID NO: 3

370 <211> LENGTH: 34

372 <212> TYPE: DNA

374 <213> ORGANISM: Artificial Sequence

378 <220> FEATURE:

380 <223> OTHER INFORMATION: Description of Artificial Sequence:

382 Oligonucleotide metAdell

386 <400> SEQUENCE: 3

388 ctatttgta gtgaataata gtactgagct ctgg

34

394 <210> SEQ ID NO: 4

396 <211> LENGTH: 34

what is this?

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/530,844

DATE: 04/19/2005

TIME: 08:46:17

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

398 <212> TYPE: DNA
 400 <213> ORGANISM: Artificial Sequence
 404 <220> FEATURE:
 406 <223> OTHER INFORMATION: Description of Artificial Sequence:
 408 Oligonucleotide metAdel2
 412 <400> SEQUENCE: 4
 414 ctggtggata tatgagatct ggtagacgta atag 34
 420 <210> SEQ ID NO: 5
 422 <211> LENGTH: 33
 424 <212> TYPE: DNA
 426 <213> ORGANISM: Artificial Sequence
 430 <220> FEATURE:
 432 <223> OTHER INFORMATION: Description of Artificial Sequence:
 434 Oligonucleotide metAext1
 438 <400> SEQUENCE: 5
 440 tgggtggatat atgagatctg gtagacgtaa tag 33
 446 <210> SEQ ID NO: 6
 448 <211> LENGTH: 34
 450 <212> TYPE: DNA
 452 <213> ORGANISM: Artificial Sequence
 456 <220> FEATURE:
 458 <223> OTHER INFORMATION: Description of Artificial Sequence:
 460 Oligonucleotide metAext2
 464 <400> SEQUENCE: 6
 466 gtatttggtta gtgaataata gtactgagct ctgg 34
 472 <210> SEQ ID NO: 7
 474 <211> LENGTH: 33
 476 <212> TYPE: DNA
 478 <213> ORGANISM: Artificial Sequence
 482 <220> FEATURE:
 484 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene
 486 Sequence
 490 <400> SEQUENCE: 7
 492 tcatatatcc accagctatt tgtagtgaa taa 33
 498 <210> SEQ ID NO: 8
 500 <211> LENGTH: 10
 502 <212> TYPE: PRT
 504 <213> ORGANISM: Artificial Sequence
 508 <220> FEATURE:
 510 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial
 512 Protein Sequence
 516 <400> SEQUENCE: 8
 518 Ser Tyr Ile His Gln Leu Phe Val Ser Glu
 520 1 5 10
 526 <210> SEQ ID NO: 9
 528 <211> LENGTH: 102
 530 <212> TYPE: DNA
 532 <213> ORGANISM: Artificial Sequence
 536 <220> FEATURE:

Same errors

What is the source of genetic material?

Partial Gene

Invalid Response

What is the source of genetic material?

Partial

Invalid Response

See item # 11 on error Summary Sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/530,844

DATE: 04/19/2005

TIME: 08:46:17

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

✓ SAME
errors

538 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene
 540 Sequence

544 <400> SEQUENCE: 9

546 tcatatatcc accactattt gtagtgaat aatagtactg agctctggat gcatacgcgt 60

550 ttaattaagc ggccgcactg cgatgagtgg cagggcgggg cg 102

556 <210> SEQ ID NO: 10

558 <211> LENGTH: 34

560 <212> TYPE: PRT

562 <213> ORGANISM: Artificial Sequence

566 <220> FEATURE:

568 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial

570 Protein Sequence

574 <400> SEQUENCE: 10

576 Ser Tyr Ile His His Tyr Leu Leu Val Asn Asn Ser Thr Glu Leu Trp

578 1 5 10 15

582 Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly

584 20 25 30

588 Gly Ala

596 <210> SEQ ID NO: 11

598 <211> LENGTH: 102

600 <212> TYPE: DNA

602 <213> ORGANISM: Artificial Sequence

606 <220> FEATURE:

608 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial Gene

610 Sequence

614 <400> SEQUENCE: 11

616 tcatatatcc accagtattt gtagtgaat aatagtactg agctctggat gcatacgcgt 60

620 ttaattaagc ggccgcactg cgatgagtgg cagggcgggg cg 102

626 <210> SEQ ID NO: 12

628 <211> LENGTH: 34

630 <212> TYPE: PRT

632 <213> ORGANISM: Artificial Sequence

636 <220> FEATURE:

638 <223> OTHER INFORMATION: Description of Artificial Sequence: Partial

640 Protein Sequence

644 <400> SEQUENCE: 12

646 Ser Tyr Ile His Gln Tyr Leu Leu Val Asn Asn Ser Thr Glu Leu Trp

648 1 5 10 15

652 Met His Thr Arg Leu Ile Lys Arg Pro His Cys Asp Glu Trp Gln Gly

654 20 25 30

658 Gly Ala

↑ See item #11
on error
summary
sheet.

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/530,844

DATE: 04/19/2005
TIME: 08:46:18

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\04192005\J530844.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,3,5,7,9,11,13,15,16,18,20,22,24,26,28,30,32,34,36,38,40
Seq#:1; Line(s) 42,44,46,48,50,52,54,56,58,60,62,64,66,68,70,72,74,76,78,80
Seq#:1; Line(s) 82,84,86,88,90,92,94,96,98,100,102,104,106,108,110,112,114
Seq#:1; Line(s) 116,118,120,122,124,126,128,130,132,134,136,138,140,142,144
Seq#:1; Line(s) 146,148,150,152,154,156,158,160,162,164,166,168,170,172,174
Seq#:1; Line(s) 176,178,180,182,184,186,188,190,192,194,196,198,200,202,204
Seq#:1; Line(s) 206,208,210,212,214,216,218,220,222,224,226,228,230,232,234
Seq#:2; Line(s) 236,238,240,242,244,246,248,250,252,254,256,258,260,262,264
Seq#:2; Line(s) 266,268,270,272,274,276,278,280,282,284,286,288,290,292,294
Seq#:2; Line(s) 296,298,300,302,304,306,308,310,312,314,316,318,320,322,324
Seq#:2; Line(s) 326,328,330,332,334,336,338,340,342,344,346,348,350,352,354
Seq#:2; Line(s) 356,358,360,362,364,366,368
Seq#:3; Line(s) 370,372,374,376,378,380,382,384,386,388,390,392,394
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Seq#:5; Line(s) 422,424,426,428,430,432,434,436,438,440,442,444,446
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Seq#:10; Line(s) 558,560,562,564,566,568,570,572,574,576,578,580,582,584
Seq#:10; Line(s) 586,588,590,592,594,596
Seq#:11; Line(s) 598,600,602,604,606,608,610,612,614,616,618,620,622,624
Seq#:11; Line(s) 626
Seq#:12; Line(s) 628,630,632,634,636,638,640,642,644,646,648,650,652,654
Seq#:12; Line(s) 656,658,660,662,664,666

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/530,844

DATE: 04/19/2005

TIME: 08:46:18

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\04192005\J530844.raw

L:18 M:270 C: Current Application Number differs, Replaced Application Number
L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:1
L:228 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1